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1

SEQUENCE LISTING

<110> CO, MAN SUNG
VASQUEZ, MAXIMILIANO
CARRENO, BEATRIZ
CELNICKER, ABBIE CHERYL
COLLINS, MARY
GOLDMAN, SAMUEL
GRAY, GARY S.
KNIGHT, ANDREA
O'HARA, DENISE
RUP, BONITA
VELDMAN, GEERTRUIDA M.

<120> HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7 MOLECULES AND METHODS OF TREATMENT THEREWITH

<130> 08702.0083-00000

<140> 09/501,102
<141> 2000-02-09

<150> 09/339,596
<151> 1999-06-24

<150> 09/249,011
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<170> PatentIn Ver. 2.1

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gtg cac tcc cag gtc cag ctg cag cag tct ggg cct gag ctg gtg agg 96
Val His Ser Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Arg
20 25 30

cct ggg gaa tca gtg aag att tcc tgc aag ggt tcc ggc tac aca ttc 144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe
35 40 45

act gat tat gct ata cag tgg gtg aag cag agt cat gca aag agt cta 192
Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac	240
Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn	
65 70 75 80	
cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc	288
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser	
85 90 95	
aca gcc tat atg gaa ctt gcc aga ttg aca tct gag gat tct gcc atc	336
Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile	
100 105 110	
tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga	384
Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly	
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Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe	
35 40 45	
Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu	
50 55 60	
Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn	
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Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser	
85 90 95	
Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile	
100 105 110	
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130 135	
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 50 55 60

 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80

 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 85 90 95

 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
 100 105 110

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 115 120 125

 Leu Glu Ile Lys
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<220>
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 1 5 10 15

gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag 96
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc tac aca ttc 144
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

act gat tat gct ata cag tgg gtg aga cag gct cct gga cag ggc ctc 192
 Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac 240
 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
 65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc	288
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser	
85	90
95	

aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtt	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100	105
110	

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt	384
Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly	
115	120
125	

acc ctt gtc acc gtc tcc tca	405
Thr Leu Val Thr Val Ser Ser	
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<211> 135

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide sequence

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30	

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35	40
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Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
50	55
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Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn	
65	70
75	80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser	
85	90
95	

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100	105
110	

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly	
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Thr Leu Val Thr Val Ser Ser	
130	135

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   1           5           10          15

ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat tcc ctg gct      96
Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
   20          25          30

gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt      144
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser
   35          40          45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag      192
Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
   50          55          60

aaa cca ggg cag cct cct aaa ctg ctg atc tac ttg gca tcc act agg      240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
   65          70          75          80

gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat      288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
   85          90          95

ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat      336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
   100         105         110

tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag      384
Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys
   115         120         125

gtg gaa ata aaa
Val Glu Ile Lys
   130

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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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 1 5 10 15
 Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
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 Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser
 35 40 45
 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65 70 75 80
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110
 Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys
 115 120 125
 Val Glu Ile Lys
 130

<210> 9
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 nucleotide sequence

<220>
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<222> (1)..(15)

<400> 9
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<222> (1)..(51)

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ggc 51
Gly

<210> 12
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<212> PRT
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<400> 12
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Gly

<210> 13
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<212> DNA
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<220>
<221> CDS
<222> (1)..(21)

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<210> 14
<211> 7
<212> PRT
<213> Mus sp.

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<400> 14
Ala Ala Trp Tyr Met Asp Tyr
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<210> 15
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gct
Ala                                         51

<210> 16
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<400> 16
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 65 70 75 80

ccg aag ttc cag ggc aag gcc agt ata aca gca gac aca tcc tcc aac 288
 Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn
 85 90 95

aca gcc tac ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc 336
 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
 100 105 110

tat tac tgt gct aga gag ggg ctt ttt ttt gct tac tgg ggc caa ggg 384
 Tyr Tyr Cys Ala Arg Glu Gly Leu Phe Phe Ala Tyr Trp Gly Gln Gly
 115 120 125

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 130 135

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<211> 135

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<213> Mus sp.

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 20 25 30

Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Pro Ser Gly Phe Asn Ile
 35 40 45

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp
 65 70 75 80

Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn
 85 90 95

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Glu Gly Leu Phe Phe Ala Tyr Trp Gly Gln Gly
 115 120 125

Thr Pro Val Thr Val Ser Ala
 130 135

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<211> 390

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 gtc ata ttg tcc agt gga gaa att gtg ctc acc cag tct cca gca ctc 96
 Val Ile Leu Ser Ser Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Leu
 20 25 30

 atg gct gca tct cca ggg gag aag gtc acc atc acc tgc agt gtc agc 144
 Met Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Val Ser
 35 40 45

 tca agt ata agt tcc agc aac ttg cac tgg tac cag cag aag tca gaa 192
 Ser Ser Ile Ser Ser Asn Leu His Trp Tyr Gln Gln Lys Ser Glu
 50 55 60

 acc tcc ccc aaa ccc tgg att tat ggc aca tcc aac ctg gct tct gga 240
 Thr Ser Pro Lys Pro Trp Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
 65 70 75 80

 gtc cct gtt cgc ttc agt ggc agt gga tct ggg acc tct tat tct ctc 288
 Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 85 90 95

 aca atc agc agc atg gag gct gaa gat gct gcc act tat tac tgt caa 336
 Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 100 105 110

 cag tgg agt agt tac cca ctc acg ttc ggt gct ggg acc aag ctg gag 384
 Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
 115 120 125

 ctg aaa
 Leu Lys 390
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<210> 24
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<213> Mus sp.

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Met Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Val Ser
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 Ser Ser Ile Ser Ser Ser Asn Leu His Trp Tyr Gln Gln Lys Ser Glu
 50 55 60
 Thr Ser Pro Lys Pro Trp Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
 65 70 75 80
 Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
 85 90 95
 Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
 100 105 110
 Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
 115 120 125
 Leu Lys
 130

<210> 25
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 <220>
 <223> Description of Artificial Sequence: Synthetic
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 gtc aat tca gag gtt cag ctg gtg cag tct ggg gct gag gtt aag aag 96
 Val Asn Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

 cca ggg gcc tca gtc aag gtg tcc tgc aaa cct tct ggc ttc aac att 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Pro Ser Gly Phe Asn Ile
 35 40 45

 aaa gac tac tat atg cac tgg gtg agg cag gcg cct gga cag ggc ctc 192
 Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

 gag tgg att gga tgg att gat cct gag aat ggt aat act cta tat gac 240
 Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp
 65 70 75 80

ccg aag ttc cag ggc aag gcc act ata act gca gac aca tcc acc agc Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Thr Ser	288	
85	90	95
aca gcc tac atg gag ctg agc agc ctg aga tct gag gac act gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	336	
100	105	110
tat tac tgt gct aga gag ggg ctt ttt ttt gct tac tgg ggc caa ggt Tyr Tyr Cys Ala Arg Glu Gly Leu Phe Phe Ala Tyr Trp Gly Gln Gly	384	
115	120	125
acc ctg gtc act gtc tct tca Thr Leu Val Thr Val Ser Ser	405	
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<210> 26

<211> 135

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<223> Description of Artificial Sequence: Synthetic peptide sequence

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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Pro Ser Gly Phe Asn Ile		
35	40	45

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu		
50	55	60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp			
65	70	75	80

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Thr Ser		
85	90	95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val		
100	105	110

Tyr Tyr Cys Ala Arg Glu Gly Leu Phe Phe Ala Tyr Trp Gly Gln Gly		
115	120	125

Thr Leu Val Thr Val Ser Ser	
130	135

<210> 27

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<212> DNA
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 <223> Description of Artificial Sequence: Synthetic
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 1 5 10 15

 gtc ata ttg tcc agt gga gat att cag atg acc cag ctc tct cca tca tcc 96
 Val Ile Leu Ser Ser Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30

 ctg tct gca tct gta ggg gat agg gtc acc atc acc tgc agt gtc agc 144
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Val Ser
 35 40 45

 tca agt ata agt tcc agc aac ttg cac tgg tac cag cag aag cca ggc 192
 Ser Ser Ile Ser Ser Asn Leu His Trp Tyr Gln Gln Lys Pro Gly
 50 55 60

 aag gcc ccc aaa ccc ttg att tat ggc aca tcc aac ctg gct tct gga 240
 Lys Ala Pro Lys Pro Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
 65 70 75 80

 gtc cct agt cgc ttc agt ggc agt gga tct ggg acc gat tat act ctc 288
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
 85 90 95

 aca atc agc agc ttg cag cct gaa gat gtt gcc act tat tac tgtcaa 336
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln
 100 105 110

 cag tgg agt agt tac cca ctc acg ttc ggt caa ggg acc aag gtc gag 384
 Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu
 115 120 125

 atc aaa
 Ile Lys 390
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 <210> 28
 <211> 130
 <212> PRT
 <213> Artificial Sequence

 <220>
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 peptide sequence

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 20 25 30
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Val Ser
 35 40 45
 Ser Ser Ile Ser Ser Ser Asn Leu His Trp Tyr Gln Gln Lys Pro Gly
 50 55 60
 Lys Ala Pro Lys Pro Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
 65 70 75 80
 Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Tyr Thr Leu
 85 90 95
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln
 100 105 110
 Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu
 115 120 125
 Ile Lys
 130

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<222> (1)..(36)

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 1 5 10

<210> 30
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<213> Mus sp.

<400> 30
 Ser Val Ser Ser Ser Ile Ser Ser Asn Leu His
 1 5 10

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<212> DNA
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<220>
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<400> 34
 Gln Gln Trp Ser Ser Tyr Pro Leu Thr
 1 5

<210> 35
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 <212> DNA
 <213> Mus sp.

<220>
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 <222> (1)...(15)

<400> 35
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Asp Tyr Tyr Met His
1 5

<210> 36
<211> 5
<212> PRT
<213> Mus sp.

<400> 36
Asp Tyr Tyr Met His
1 5

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<220>
<221> CDS
<222> (1)..(51)

<400> 37
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ggc 51
Gly

<210> 38
<211> 17
<212> PRT
<213> Mus sp.

<400> 38
Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 39
<211> 21
<212> DNA
<213> Mus sp.

<220>
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<222> (1)..(21)

<400> 39
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Glu Gly Leu Phe Phe Ala Tyr
1 5

21

<210> 40
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<212> PRT
<213> Mus sp.

<400> 40
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1 5